Amendments to the Claims:

This listing of the claims will replace all prior versions, and listings, of claims in the application:

Listing of Claims:

1. (Currently amended) A method for detecting a mutation, comprising: a) amplifying a target polynucleotide using a forward primer and a reverse primer to produce an amplified target polynucleotide; b) contacting said amplified target polynucleotide with two or more restriction endonucleases to generate at least one restriction fragment, said restriction fragment comprising two single-stranded fragments of 2-32 nucleotides each, wherein ~~at least one~~ both of said single-stranded ~~fragment~~ fragments contains [[a]] at least one mutation sequence, said mutation sequence being a base substitution, deletion or insertion; [[and]] c) measuring the molecular weights of said single-stranded fragments, and d) comparing said molecular weights of said single-stranded fragments to the molecular weights of control fragments, wherein if said molecular weights of said single-stranded fragments differs from the molecular weights of said control fragments, said mutation is detected.

2. (Currently amended) The method according to claim 1, wherein said restriction fragment comprising two single-stranded fragments includes one mutation among two or more different mutations in only one of said single stranded fragment and all ~~other~~ mutations including said one mutation in the other said single stranded fragment.

3. (Original) A method for detecting a mutation, comprising: a) amplifying a target polynucleotide using a forward primer and a reverse primer to produce an amplified target polynucleotide; b) cleaving the amplified target polynucleotide using a first restriction endonuclease and a second restriction endonuclease, under conditions in which said second restriction endonuclease does not cleave said amplified target polynucleotide; c) cleaving the product of step b) under conditions in which said second restriction endonuclease cleaves said amplified target polynucleotide to produce a plurality of restriction fragments that comprise single-stranded fragments; d) measuring the molecular weight of said single-stranded fragments; and e) comparing said molecular weights of said single-stranded fragments to the molecular weights of control fragments, wherein if said molecular weights of said single-stranded fragments differs from the molecular weights of said control fragments, said mutation is detected.

4. (Original) The method according to claim 1, wherein said contacting is performed using restriction endonucleases having different optimum temperatures.

5. (Original) The method according to claim 3, wherein said first restriction endonuclease has a different optimum temperature than said second restriction endonuclease.

6. (Original) The method according to claim 4, wherein a first restriction endonuclease is selected from the group consisting of *Fok*1, *Bbv*I, *Bsg*I, *Bcg*I, *Bpm*I, *Bse*RI and *Bae*I, and a second restriction enzyme is selected from the group consisting of *Bst*F5I, *Taq*I, *Bsa*BI, *Btr*I, *Bst*API, *Fau*I, *Bcl*I, *Pci*I and *Apo*I.

7. (Original) The method according to claim 5, wherein said first restriction endonuclease is selected from the group consisting of *Fok*1, *Bbv*I, *Bsg*I, *Bcg*I, *Bpm*I, *Bse*RI and *Bae*I, and a second restriction enzyme is selected from the group consisting of *Bst*F5I, *Taq*I, *Bsa*BI, *Btr*I, *Bst*API, *Fau*I, *Bcl*I, *Pci*I and *Apo*I.

8. (Currently amended) The method according to claim 1, wherein said amplified target polynucleotide comprises a polynucleotide sequence encoding a tyrosine-methionine-aspartate-aspartate (YMDD) site which is an active site of DNA polymerase of hepatitis B virus.

9. (Currently amended) The method according to claim 3, wherein said amplified target polynucleotide comprises a polynucleotide sequence encoding a tyrosine-methionine-aspartate-aspartate (YMDD) site which is an active site of DNA polymerase of hepatitis B virus.

10. (Original) The method according to claim 1, wherein said amplified target polynucleotide comprises a 5'-NCR (non-coding region) site of a hepatitis C virus.

11. (Original) The method according to claim 3, wherein said amplified target polynucleotide comprises 5'-NCR (non-coding region) site of a hepatitis C virus.

12.-16. (Canceled)